

FIG. 2

3/13

Sgl-TcmO	173	FVDLGGARG	234	PRADVFI	263	ALTPGGAVLV
Sgl-TcmN	331	IADLGGGDG	393	TGYDAYLF	423	IGDDDDARLLI
Smy-MdmC	64	VLEIGTFTG	135	GAFDIVEV	159	LVRPGGLVAI
Mxa-SafC	63	TLEVGVTFTG	134	GTFDLAFI	158	LVRPGGLIIL
Ser-EryG	85	VLDVGFGLG	149	ETEDRVTS	178	VLKPGGVLA
Spe-DauK	183	VLDVGGGKG	254	RKADAAIL	273	ALEPGGRILI
Sal-DmpM	208	VVDIGGADG	269	GGDLIVL	298	AMPAHARLLV
Shy-RapM	106	VLEVGCGMG	155	VQDAEEL	194	ALRRGGALSH
Sav-AveD	71	VLDVCGGSG	124	GSEDAAWA	151	VLRPGGRLAV
Sar-Cmet	158	VLDVACGHG	220	GPYDLSLI	251	ATRPGGRIGI
AlbII	174	VLDVAAGHG	236	SGYDVILL	267	ALNDDGMVIT
		Motif I		Motif II		Motif III

FIG. 3

Sgl-tcmP	84	VVLHLACGLDSRAFRMDVPD109	DVDVPDVIELR	139	EDWLDTVF	150	PALVVAEGLTPYL
Sme-PKS	84	TVLHLGCGLDSRIFRIDPGP109	ELDVPDVISLR	139	RGWIERLP	150	PTMIVAEGVLPYL
Pmu-tcmP	86	VVVLGAGLDARFERLGKQP111	DLDLPEVINIR	141	TDMMKTVS	152	PVLLILEGVLMFF
Mtu-Omt	85	TVVALAEGLOTSEWRDLDAI113	TVDLPPIVDLR	144	YSWMDSDV	155	GVFITAEGLLMYL
Mlo-Hp	84	IVLHLGCGLDTRVFRVDP109	DADYPQVIELR	139	PGWLAIEVP	150	PAMVVAEGLTPYL
Mtu-Hp	101	QVAILASGLDSRAYRLPWPT127	EIDQPKVMEFK	162	ADWPTALQ	178	PTAWLAEGLLIYL
Mtu-Hp2	104	QVVILASGLDSRAWRLPWP129	ELDQPKVLEFK	162	QDWPKALQ	178	PCAWLAEGLVRYL
Mtu-Hp3	98	QVVILAGLDSRAYRLPWP123	ELDRPQVLDFK	156	DDWPOALR	172	PSAWIAEGLLIYL
Mtu-Hp4	101	QAVIVAAGLDCRAYRLDWQ126	EIDVPKVLEFK	161	TDWPTPLT	177	PSAWSVEGLLPYL
Sco-Hp	93	QVVLGAGMDSRAFRMAWPE118	EVDTPAPLEFK	153	EDWPSALA	169	PTAWIGEGLLIYL
AlbVI	99	QVVILAGMDARAYRLPWPS124	EIDHMDVLSDK	157	EDWPOALK	173	ATLWLVEGLLCYL
		Motif I		Motif II		Motif III	Motif IV

FIG. 4

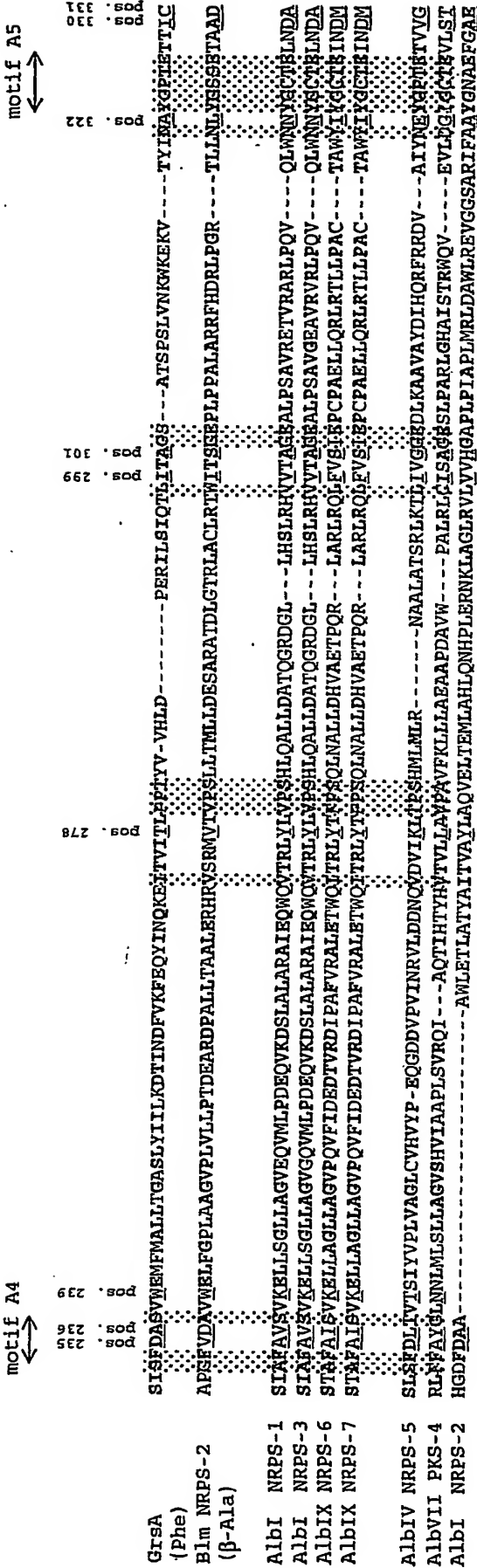


FIG. 5

XALB1 Strand +									
29 bp downstream from the TGA stop codon of <i>albXVII</i>									
-40	-35	-30	-25	-20	-15	-10	-5	-1+	+5
.
17085=>	ACCATGTGTAACGGCCTTCCCGCTTCGTCATAGCGATTTTCGATCGGGC	4.30	0						
XALB1 Strand +									
400 bp downstream from the TAA stop codon of <i>albIV</i>									
-40	-35	-30	-25	-20	-15	-10	-5	-1+	+5
.
55617=>	CATGGCTGCAGGCCGAGCTCGCTCAGCTACGGGTGAGACCGAAGCTGCCC	4.13	12						
XALB1 Strand -									
62 bp, 170 bp and 560 bp downstream from the TAG stop codon of <i>albXVI</i>									
-40	-35	-30	-25	-20	-15	-10	-5	-1+	+5
.
7030=>	GGGGGCGCAGTTGCCCGGACCCCGGTTTCTGTAAACGTTTGGCTGTCTGTAG	3.95	13						
XALB3 Strand +									
8065=> GCAAGAAAAGCGGAACGAAAAAGGCCCTACGGGCCCTTTTCTTCCA									
8072=> AAAGCGGAACGAAAAAGGCCCTACGGGCCCTTTTCTTCCATCGTCA									

14456 GTCGTTGATCAGCACCATAGCCTGTTCTCTGAACCTCATCTCTAAAGATACCCCGGAAGCTGCTGCGAAGCACGGAAGTTGCTACATCGCAC
CAGCAACTAGTCGTGGTCTATTTCGGACAAGGAGCTTCAGTAGGATTTCATGGGGGCCCTTCGGACGACGCTTCGTGCCCTTCAACGATGTAGCGTG
D N I L V L Y A Q E E F T M RBS
albX
-35 (PalbX: operon 3) -10 (PalbX: operon 3)
14552 AATGCGATTGAGATGGACCAAGCAAGCGACTATATACATGACGTCACCTTCGAGATGTCAAGAAAAATAGCCGCTGAAGAGCACGTAAGAGTGATGT
TTACGCTAAGTCTACCTGGTTTCGTTTCGCTGATATGTAAGTGTGAGTGAAGCTTCTACAGTTCTTTTTTATCGCGCACCTTCTCGTGCATTCTCACTACA
-10 (PalbXVII: operon 4) -35 (PalbXVII: operon4)
14648 GTTTCGCACCGCTGTACGTCCTCCATCGCCATCGCGGGCAAGCTTACACGAAAAATTCACGAGGGCATCGGTTCAATACGCGGGTCAAAGCAATATCC
CAAAGCGTGGCGACATGCAGGGTAGCGGTAGCGCCGTTTCGAATGTGCTTTTAAAGTGGTCCCGTACGCAAGTTATGCGGCCAGTTTCGTTATAGG
14744 TTGGGCTTGCAGAGCTATGTTCTGTCGTAAAGCGCCCAAGCAGTGGGGAGCAACACCTTGGGTTTCGGTTGAGGTGCGGGTAGCAATTCTCTGCTTA
AAGCGAACGTCCTCGATACAAAGCAGGCATTTTCGGGGTTCGGTCAACCCCTCGTTGTGGAAACCAAGCCAACTCCACGCCCATCGTTAAAGACGAAT
RBS
14840 ATATCCACGCGCGGGGTTTTGTCTTGCCGGGGGTCAACTGTCTCATCGAGCAGTCTGGGAGGCTATTTTGGCGTGCCTTATCATAAATAATTAC
TATAGGTGCGCGCGCCGCAAAAACAGAACGCGCCCGCAGTTGACAGAGTAGCTCGTCAGACCCCTCCGATAAAACGCGACGGAATAGTATTATTAAATG
M R C L I I N N Y
albXVII

FIG. 7A

17332 GAATAGGCCCCACGCTTACGCGCGAACCAGGACGGGCTGCTGATGATACGGCCGGCGGTGGTCGAGGGCTGCACCAGCAATCTGTTCCCTCG
CTTACTCCGGGGGTGCGAATGCGCGCTTGGTCCCTGCCCGACGACTACCTATGCCGGCCGCCACCAGCTCCCGACGTGGTCGTTAGACAAGGAGC
M R P P R L R A N Q D G L
albVIII (non expressed ?)

17428 TCGAGAACGGCCCATCTGGTGACGCCCGGACCTGGGCGTGGCCGGCTACGGGGATCATGCGAGGCGGGTGATCGAATATGGCCGGCAGCAGGTC
AGCTCTTGCCGGTAGACCACTGCGGGCTGGACCCGACCGCGCAGTCGCCCTAGTAGCGTCCGTCCCAGTAGCTTATACCGGCCGTCGTGCCAG

17524 TCGCCTGCGCGGTAAAGCACGCTCTATCCGGACCAAGTAGTGCCTGCTCAGAGGTTGTTCTGACTAACGCCGTGTTCCGGCATTTCTGCTGGTGGCA
AGCGGACGCGCCATTTCGTGCAGATAGGCCCTGGTCGATCAGGCACGAGTCTCCACAAAGACTGATTGCGGCACAAAGCCGTAAAGACGACCAACGCGT
-35 (PalbXIX: operon 5) -10 (PalbXIX: operon 5)
17620 GCATTGACGCTCACAGCTACCGCATCGATCCTGTTACCCCTGCGTTTGGTCGATGCCCTGTGTCAAGGGCGTATATTTACCGAAGCGGTCACTACATC
CGTAACTGCGAGTGTGATGGCGTAGCTAGGACAAATGGGACGCAACGAGCTACGGGACACAGTCCCGCATATAAAGTGGCTTGCCAGTGATGTAG

RBS
17716 AGGTTTCCACCCATGCCGCGCAAGACCCCTTGAAAGCAAGGATTACTGTGGAGAAAAGCTTCGTCAAGGAAAGATCGCTCCGGGCAATCGCTGGAGTCG
TCCAAAGGTGGGTACGGCCGGTTCTGGGAACCTTTCGTTCCCTAATGACACCTCTTTTGAAGCAGTCGCTTCTAGCGAGGCCCGGTTAGCGACCTCAGC
M P A K L E S K D Y C G E S F V S
albXIX

FIG. 7B

XALB2

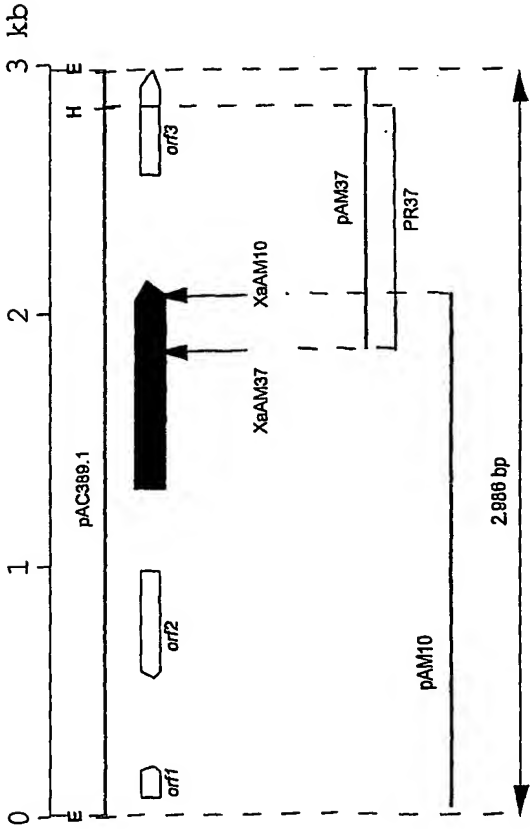
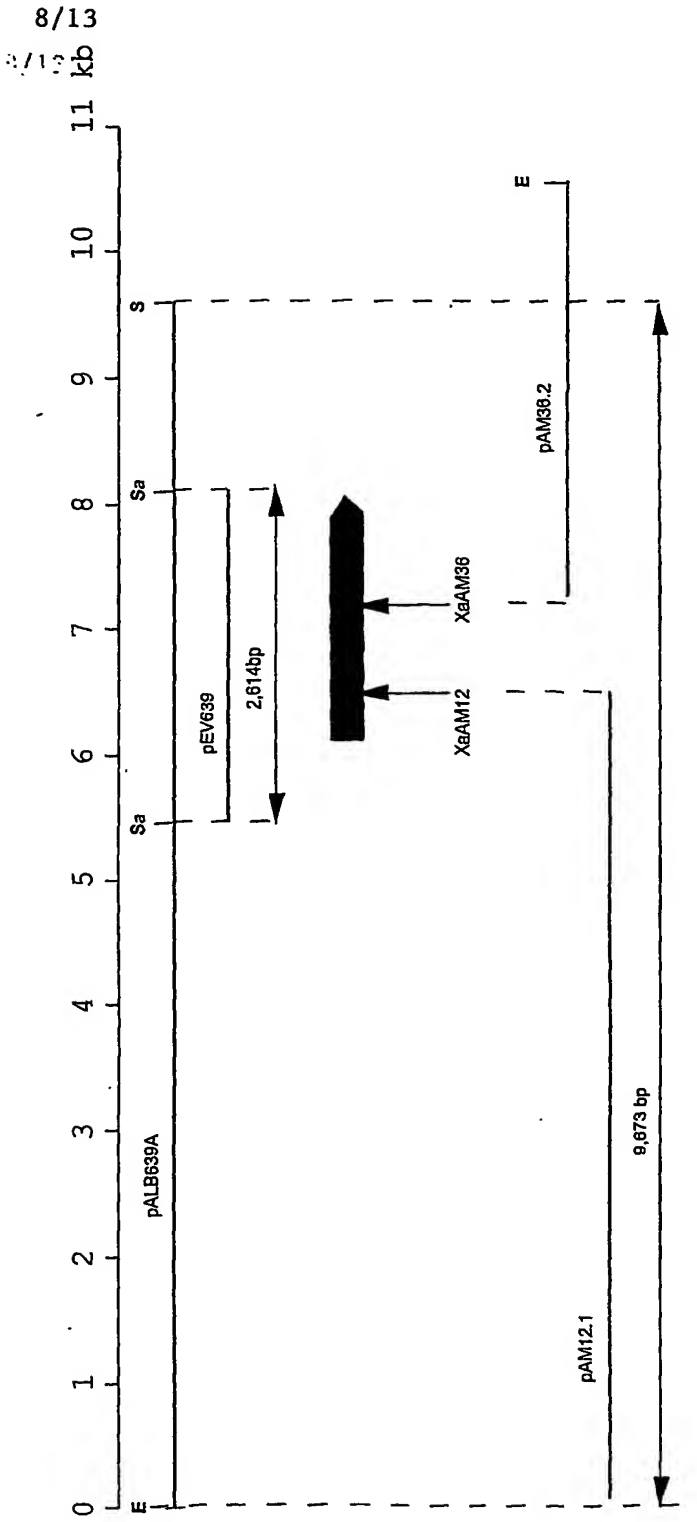


FIG. 8

XALB3



9/13

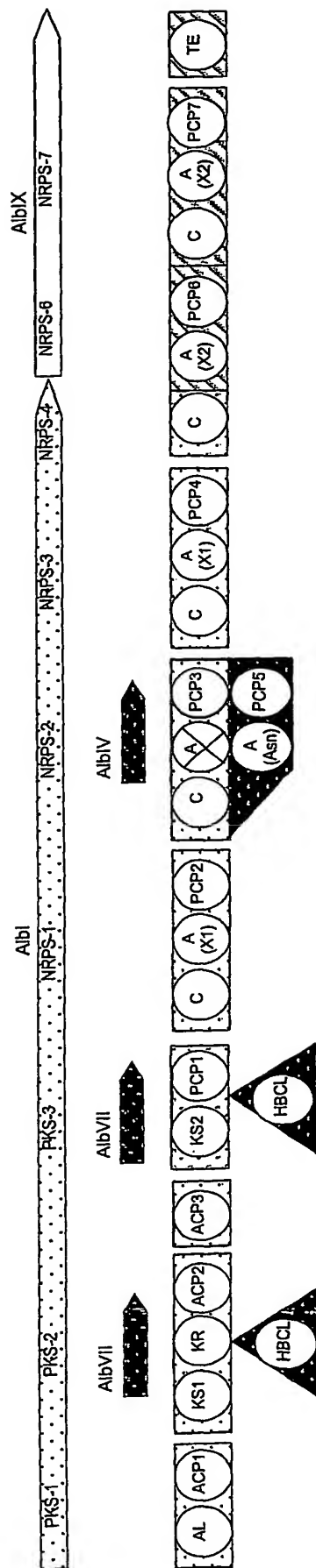


FIG. 9A

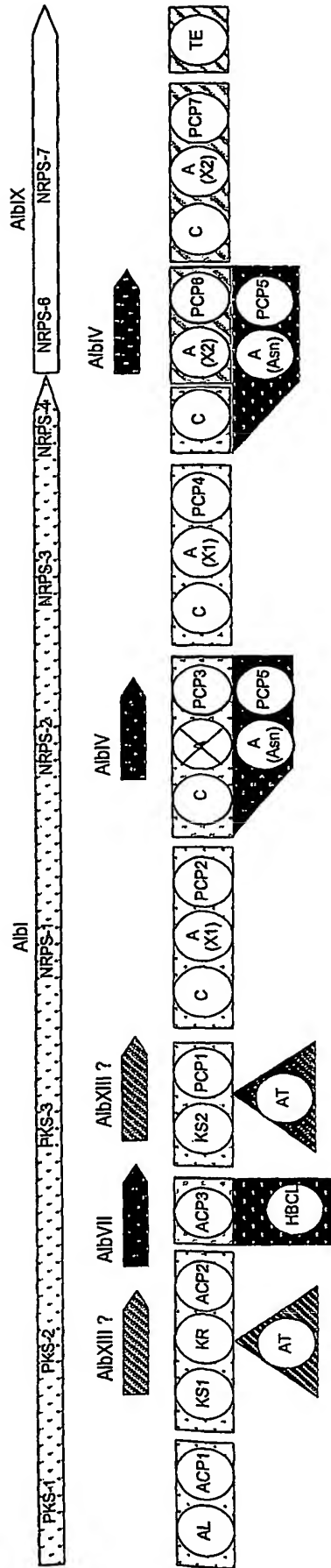


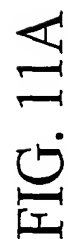
FIG. 9B

RiFa-1 LGRVDVLQPACFAVMVGGLAAVWESVGVRPDAVVGHSQGEI
RiFa-2 LDQMTYTQGALFAVETALFRLEFESWGVRRPGLLAGHSIGEL
RiFa-3 LDRVDVVQPASFAMMVGLAAVWTSIGVTPDAVLGHSQGEI
RiFB-1 LDRVDVVQPASFAVMVGGLAAVWESVGVRPDAVVGHSQGEI
RiFE-1 LNQTVFTGAGLFAVESALFRLAESWGVRRPDVVLGHSIGEI
BlmVIII ADDTRAAQPALFAVEYALARTLMDWGVRRPAPAMLGHSLGEV

FIG. 10A

AlbXIII LEDRPRHIRAVIDTLTGHAQFGPAIQAHNVAVIGHSVGGY
FenF TRTMNAQPAILTVSVIAYQVYMQEIGIKPHFLAGHSLGEY
LipA PDSRGRQLLAALDYL TGRSSVRGRIDSGRLGVMGHSMMGGG

FIG. 10B



12/13

$C_{40}O_{15}N_6H_{35}$
(molecular weight : 839)

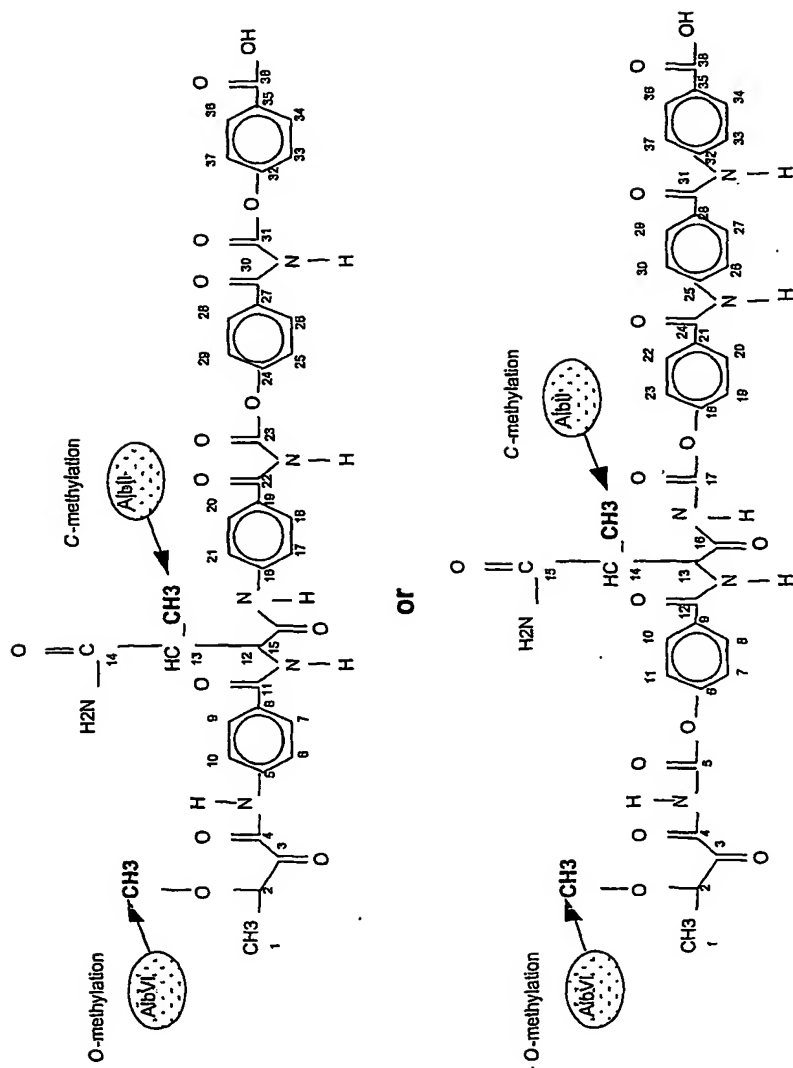


FIG. 11B

